Cycle E: Computational and Systems Biology

Coordinator: Richard Neher

The seminar series "Current Research in Bioinformatics" and "Making of a Drug" are suited for listeners without a detailed computational background. "Programming for life sciences "consists of lectures and exercises, where students are expected to acquire programming skills to be able to solve data analysis problems in life sciences. "Theoretical Biophysics" and "Computational Systems Biology" make the students familiar with current topics in these sub-fields. Basic programming skills and a solid mathematical background are required. For students interested in computational biology, but without a background in computational sciences, the lecture Computational Biology I is worth attending, but it is not part of the graduate teaching program. Similarly, the block course in Synthetic Systems Biology is recommended to students with basic molecular biology skills and interest in this topic.

E1: Current research in Bioinformatics I – 22830
(2 hrs/week, 1 CP; Fall 2019, Lecture series with invited speakers)

E2: Current research in Bioinformatics II – 21563
 (2 hrs/week, 1 CP; Spring 2020, Lecture series with invited speakers)

A. Becskei, **R. Neher**, T. Schwede, E. v. Nimwegen, M. Zavolan

Computational biology and bioinformatics methodologies have become integral to molecular biology research in the post-genomics era. Developments are taking place at a staggering pace in all areas, from genomic sequence analysis to the analysis of phenotypes with imaging techniques. This course aims to expose the students to current directions of active research in computational and systems biology and bioinformatics.

E3: Programming for Life Science – 43513
(2 hrs/week, 4 CP; Fall 2019, Practical course with exercises to be solved at home)

G. Fucile, T. Schwede, **M. Zavolan**

Together with new measurement technologies, the use of computational and mathematical approaches that exploit modern information technology in the study of biological systems have brought about a deep transformation in the practice of molecular biology research. To take advantage of the new opportunities, the new generation of biologists should be highly competent not only in their experimental work but also in the development and use of mathematical and computational methods. This course aims to train the students into the proficient use of programming in analyzing data derived from projects in life sciences. The course is focused on the widely used Python programming language, with a few examples from other commonly used languages such as R and Matlab.

E4: Computational Systems Biology – 25661
(3 hrs/week + exercises, 6 CP; Fall 2019, Lecture and exercises)

R. Neher, **E. v. Nimwegen**, M. Zavolan

Systems Biology has established itself in the past ten - fifteen years as the field in which large-scale quantitative measurements at multiple levels are analyzed in the context of mathematical models to reach a better, more predictive understanding of biological systems. This lecture provides an introduction to current topics and methods in computational systems biology. It will introduce the student to topics ranging from evolution and scaling laws in biological systems to quantitative approaches that employ biophysical methods with the aim of building an understanding of how the behavior biological systems can be described quantitatively. Pre-requisites are a good mathematical background (e.g. acquired through the Computational Biology I and II lecture series) as well as basic training in biology.

E5: Theoretical biophysics – 49038
(2 hrs/week 4 CP; Fall 2020)

R. Neher

This course will cover concepts of theoretical biophysics and introduce mathematical and numerical methods to solve problems in quantitative biology. In particular, we will focus on polymer physics, membranes, diffusion in different dimensions, electrostatic interactions, and self-organization within cells.
During the course, the students will learn techniques of quantitative reasoning such as dimensional analysis and methods for approximate analytic solutions of difficult mathematical problems (dominant balance, saddle point approximations, integral transforms, iteration techniques, etc.). Problems will be tackled both analytically to understand the qualitative behavior of a system and numerically to obtain quantitative predictions.

Prerequisites:
- Basic calculus and linear algebra
- Basics of scientific computing and numerical mathematics
- Basic programming skills (preferably Python)

E7: Introduction to R – 48662
(2 hrs/week, 2 CP; Fall 2019, Lecture and exercises)

L. Burger, F. Geier, **R. Ivanek**, P. Papasaikas, J. Roux, A. Sethi, Ch. Soneson, M. Stadler

R is a free software and it became the main programming language in bioinformatics and statistics. This lecture series teaches you basic knowledge of R and how to use it in order to explore and visualize data and perform basic statistical analysis. Each session consists of 1-hour lecture and 1 hour hands on practical. Participants should bring along their laptops.

E8: Analysis of genomics data with R/Bioconductor – 45038
(2 hrs/week, 2 CP; Spring 2020, Lecture and exercises)

S. Carl, F. Geier, **R. Ivanek**, J. Roux, A. Sethi, M. Stadler

The R/Bioconductor framework is the most widely used analysis tool for sequence-based bioinformatics. The lecture gives an overview of typical Bioconductor based analysis pipelines including:
 – Microarray and NGS data processing
 – Differential gene expression analysis
 – Working with sequence and annotation packages
 – Programmatic access to public databases
 – Visualization of genomic data

Each lecture is organized around one analysis question using publicly available data. It consists of 1-hour lecture and 1 hour hands on practical. Participants should bring along their laptops. Basic R knowledge is of an advantage.

E9: Computational Biology II – Sequence Modeling and Analysis – 27247
(2 hrs/week, plus 1h exercises; 4 CP; Spring 2020, Lectures and Exercises)

M. Zavolan

The course is the continuation of the Computational Biology I lecture. Students are introduced to more sophisticated computational biology applications. The following topics are usually covered:
 – Evolution: Mathematical models for the evolution of DNA sequences.
 – Phylogenies: the evolutionary relationships between sequences.
 – Alignment of sequences: finding corresponding positions.
 – Functional annotation: Finding genes and regulatory sequences.
 – Families of coding sequences: Hidden Markov models of protein domains
 – Gene expression networks
 – Metabolic networks

Students should have a good understanding of calculus, linear algebra, combinatorics and algorithms and should be familiar with concepts of molecular biology.

E10: Making of a Drug – 52327
(2 hrs/week, 2 CP; Fall 2019, Lecture series with speakers from industry and academia)

D. Hoepfner, **T. Schwede**

The "Making of a drug" is an endeavor that usually takes 15 years or more, involves hundreds of scientists, and consumes a budget of more than 2 billion Swiss Francs on average. No single individual is an expert on all aspects of such a project complex and challenging project. It requires resilience, engagement and team spirit with deep scientific commitment on a global scale. However, a fundamental understanding, by everyone involved, of the problems encountered along the way is considered a key ingredient for success.

Recommended lectures *outside* the graduate teaching program:

Block course on synthetic systems biology:
Biotechnological Microbiology II – 12469
(3-week block course, 8 CP; Fall 2019)
A. Becskei

→ 1-2 students could take part, depending on space availability. If you are interested, please contact A. Becskei.

The course covers concepts of synthetic gene regulatory networks in microorganisms. The relevant molecular biological mechanisms are discussed, followed by the kinetic description of these mechanisms. Subsequently, experiments are performed that demonstrate network behavior including cellular memory, bell-shaped response and stochastic gene expression.
By the ends of the course, the students will be able to write up, solve and analyze basic equations describing gene regulatory mechanisms. Furthermore, students will be able to construct synthetic gene regulatory networks for specific behaviors.

Computational Biology I – 23605
(2 hrs/week, 4 CP; Spring 2020)
E. v. Nimwegen

→ This course is part of the BSc Biology and BSc Computational Sciences, and can therefore only be counted to the Wahlbereich. (Of course only for those who have not attended it during their BSc!)

This course provides a general introduction into quantitative analysis of data. Students will be introduced to the modern view of probability theory as a general method for reasoning with incomplete information and, guided by practical examples taken from computational biology, will get acquainted with the most important concepts and methods used in statistical analysis and modeling of data. By the end of the course students should have gained a solid understanding of the fundamentals of probabilistic analysis, and how to apply it to analyze biological data. The course also acts to introduce the probabilistic methods which are used in the more sophisticated computational biology applications that are presented in the course Computational Biology II (27247).

Students should fulfil the following prerequisites:
- Mathematics Background:
  Although no formal requirements are made, the course assumes that students are comfortable with mathematical methods including analysis, calculus, and linear algebra, at a fairly advanced level.
- Computer Science Background
  Although not necessarily required, familiarity with the basics of programming is helpful.